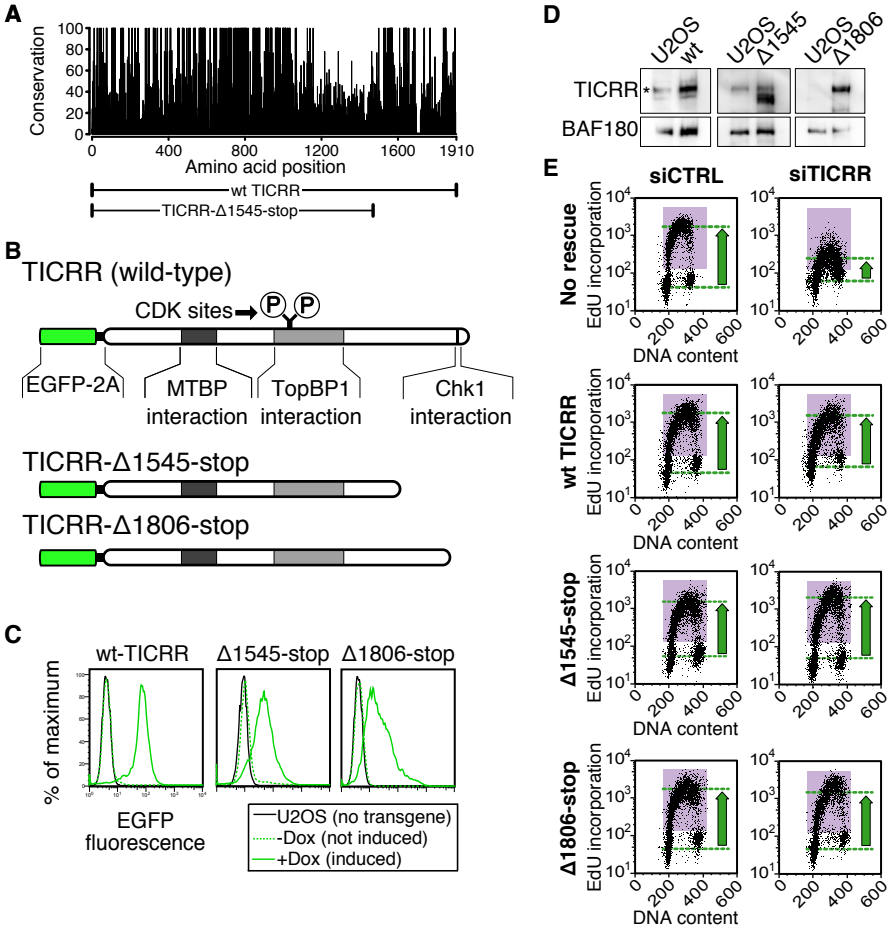

Fig. S1. The highly conserved TICRR C-terminus is not required for DNA synthesis. (A) Graph of amino acid sequence conservation for vertebrate TICRR sequences (*D. rerio* NP_001003887.1, *L. oculatus* XP_015199275.1, *X. laevis* NP_001165777, *G. gallus* NP_001272798, *H. sapiens* NP_689472.3). **(B)** Schematic of TICRR constructs. All constructs had synonymous mutations that confer resistance to TICRR siRNA. EGFP fused to the TICRR mRNA *via* a self-cleaving viral 2A peptide sequence was used to monitor expression. The TICRR-Δ1545-stop construct lacked the conserved portion of the C-terminus, including the amino acids necessary for the Chk1 interaction. The TICRR-Δ1806-stop mutant lacked the Chk1 interaction sequence. **(C)** All transgenic clones were tested for uniform EGFP-2A-TICRR expression using FACS analysis of single-cell EGFP fluorescence. **(D)** Western blotting to confirm expression of the TICRR transgenes in nuclear lysates. The TICRR antibody detected both endogenous (*) and transfected protein. BAF180 was used as a loading control. **(E)** EdU incorporation and DNA content following siRNA knockdown of TICRR. Representative plots of FACS data quantified in Fig. 1 C,D are shown.